

OIKE

RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/806,703A

TIME: 15:05:16

Input Set : A:\2001-11-13 3631-0109P CRF.txt

Output Set: N:\CRF3\11162001\I806703A.raw

ENTERED

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3 <110> APPLICANT: Steinaa, Lucilla
4      Mouritsen, Soren
5      Gautam, Anand
6      Dalum, Iben
7      Haaning, Jesper
8      Leach, Dana
9      Nielsen, Klaus
10     Karlsson, Gunilla
11     Rasmussen, Peter
13 <120> TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
15 <130> FILE REFERENCE: 3631-0109P
17 <140> CURRENT APPLICATION NUMBER: US 09/806,703A
18 <141> CURRENT FILING DATE: 2001-04-04
20 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00525
21 <151> PRIOR FILING DATE: 1999-10-05
23 <150> PRIOR APPLICATION NUMBER: DK 1998 01261
24 <151> PRIOR FILING DATE: 1998-10-05
26 <150> PRIOR APPLICATION NUMBER: US 60/105,011
27 <151> PRIOR FILING DATE: 1998-10-20
29 <160> NUMBER OF SEQ ID NOS: 41
31 <170> SOFTWARE: PatentIn Ver. 3.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2253
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
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39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(2253)
41 <223> OTHER INFORMATION:
43 <220> FEATURE:
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45 <222> LOCATION: (58)..(2253)
46 <223> OTHER INFORMATION: Human PSM'
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51 1          5          10          15
52 cgc ccg cgc tgg ctg tgc gct ggg gcg ctg gtg ctg gcg ggt ggc ttc      96
53 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
54          20          25          30
55 ttt ctc ctc ggc ttc ctc ttc ggg tgg ttt ata aaa tcc tcc aat gaa      144
56 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
57          35          40          45
58 gct act aac att act cca aag cat aat atg aaa gca ttt ttg gat gaa      192
59 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
60          50          55          60
61 ttg aaa gct gag aac atc aag aag ttc tta tat aat ttt aca cag ata      240

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62	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr	Asn	Phe	Thr	Gln	Ile	
63	65					70				75					80		
64	cca	cat	tta	gca	gga	aca	gaa	caa	aac	ttt	cag	ctt	gca	aag	caa	att	288
65	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	Gln	Leu	Ala	Lys	Gln	Ile	
66					85					90					95		
67	caa	tcc	cag	tgg	aaa	gaa	ttt	ggc	ctg	gat	tct	gtt	gag	cta	gca	cat	336
68	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	Asp	Ser	Val	Glu	Leu	Ala	His	
69				100					105				110				
70	tat	gat	gtc	ctg	ttg	tcc	tac	cca	aat	aag	act	cat	ccc	aac	tac	atc	384
71	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	
72			115					120					125				
73	tca	ata	att	aat	gaa	gat	gga	aat	gag	att	ttc	aac	aca	tca	tta	ttt	432
74	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	
75		130					135				140						
76	gaa	cca	cct	cct	cca	gga	tat	gaa	aat	gtt	tgc	gat	att	gta	cca	cct	480
77	Glu	Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	
78	145				150					155					160		
79	ttc	agt	gct	ttc	tct	cct	caa	gga	atg	cca	gag	ggc	gat	cta	gtg	tat	528
80	Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	
81				165					170				175				
82	gtt	aac	tat	gca	cga	act	gaa	gac	ttc	ttt	aaa	ttg	gaa	cgg	gac	atg	576
83	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	
84			180					185					190				
85	aaa	atc	aat	tgc	tct	ggg	aaa	att	gta	att	gcc	aga	tat	ggg	aaa	gtt	624
86	Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	
87			195					200					205				
88	ttc	aga	gga	aat	aag	gtt	aaa	aat	gcc	cag	ctg	gca	ggg	gcc	aaa	gga	672
89	Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	
90		210				215						220					
91	gtc	att	ctc	tac	tcc	gac	cct	gct	gac	tac	ttt	gct	cct	ggg	gtg	aag	720
92	Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
93	225				230					235					240		
94	tcc	tat	cca	gat	ggt	tgg	aat	ctt	cct	gga	ggt	ggt	gtc	cag	cgt	gga	768
95	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly	
96				245				250				255					
97	aat	atc	cta	aat	ctg	aat	ggt	gca	gga	gac	cct	ctc	aca	cca	ggt	tac	816
98	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	
99			260					265				270					
100	cca	gca	aat	gaa	tat	gct	tat	agg	cgt	gga	att	gca	gag	gct	gtt	ggt	864
101	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly	
102			275					280				285					
103	ctt	cca	agt	att	cct	gtt	cat	cca	att	gga	tac	tat	gat	gca	cag	aag	912
104	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys	
105		290				295				300							
106	ctc	cta	gaa	aaa	atg	ggt	ggc	tca	gca	cca	cca	gat	agc	agc	tgg	aga	960
107	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg	
108	305				310					315					320		
109	gga	agt	ctc	aaa	gtg	ccc	tac	aat	gtt	gga	cct	ggc	ttt	act	gga	aac	1008
110	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn	

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111		325		330		335	
112	ttt tct aca caa aaa gtc aag atg cac atc cac tct acc aat gaa gtg						1056
113	Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val						
114		340		345		350	
115	aca aga att tac aat gtg ata ggt act ctc aga gga gca gtg gaa cca						1104
116	Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro						
117		355		360		365	
118	gac aga tat gtc att ctg gga ggt cac cgg gac tca tgg gtg ttt ggt						1152
119	Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly						
120		370		375		380	
121	ggt att gac cct cag agt gga gca gct gtt gtt cat gaa att gtg agg						1200
122	Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg						
123	385		390		395	400	
124	agc ttt gga aca ctg aaa aag gaa ggg tgg aga cct aga aga aca att						1248
125	Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile						
126		405		410		415	
127	ttg ttt gca agc tgg gat gca gaa gaa ttt ggt ctt ctt ggt tct act						1296
128	Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr						
129		420		425		430	
130	gag tgg gca gag gag aat tca aga ctc ctt caa gag cgt ggc gtg gct						1344
131	Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala						
132		435		440		445	
133	tat att aat gct gac tca tct ata gaa gga aac tac act ctg aga gtt						1392
134	Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val						
135		450		455		460	
136	gat tgt aca ccg ctg atg tac agc ttg gta cac aac cta aca aaa gag						1440
137	Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu						
138	465		470		475	480	
139	ctg aaa agc cct gat gaa ggc ttt gaa ggc aaa tct ctt tat gaa agt						1488
140	Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser						
141		485		490		495	
142	tgg act aaa aaa agt cct tcc cca gag ttc agt ggc atg ccc agg ata						1536
143	Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile						
144		500		505		510	
145	agc aaa ttg gga tct gga aat gat ttt gag gtg ttc ttc caa cga ctt						1584
146	Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu						
147		515		520		525	
148	gga att gct tca ggc aga gca cgg tat act aaa aat tgg gaa aca aac						1632
149	Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn						
150		530		535		540	
151	aaa ttc agc ggc tat cca ctg tat cac agt gtc tat gaa aca tat gag						1680
152	Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu						
153	545		550		555	560	
154	ttg gtg gaa aag ttt tat gat cca atg ttt aaa tat cac ctc act gtg						1728
155	Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val						
156		565		570		575	
157	gcc cag gtt cga gga ggg atg gtg ttt gag cta gcc aat tcc ata gtg						1776
158	Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val						
159		580		585		590	

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160 ctc cct ttt gat tgt cga gat tat gct gta gtt tta aga aag tat gct      1824
161 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
162          595          600          605
163 gac aaa atc tac agt att tct atg aaa cat cca cag gaa atg aag aca      1872
164 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
165          610          615          620
166 tac agt gta tca ttt gat tca ctt ttt tct gca gta aag aat ttt aca      1920
167 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
168 625          630          635          640
169 gaa att gct tcc aag ttc agt gag aga ctc cag gac ttt gac aaa agc      1968
170 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
171          645          650          655
172 aac cca ata gta tta aga atg atg aat gat caa ctc atg ttt ctg gaa      2016
173 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
174          660          665          670
175 aga gca ttt att gat cca tta ggg tta cca gac agg cct ttt tat agg      2064
176 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
177          675          680          685
178 cat gtc atc tat gct cca agc agc cac aac aag tat gca ggg gag tca      2112
179 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
180          690          695          700
181 ttc cca gga att tat gat gct ctg ttt gat att gaa agc aaa gtg gac      2160
182 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
183 705          710          715          720
184 cct tcc aag gcc tgg gga gaa gtg aag aga cag att tat gtt gca gcc      2208
185 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
186          725          730          735
187 ttc aca gtg cag gca gct gca gag act ttg agt gaa gta gcc taa      2253
188 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
189          740          745          750
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193 <211> LENGTH: 750
194 <212> TYPE: PRT
195 <213> ORGANISM: Homo sapiens
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (2)..(2)
200 <223> OTHER INFORMATION: The 'Xaa' at location 2 stands for Gly or Trp.
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205 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
206          20          25          30
207 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
208          35          40          45
209 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
210          50          55          60
211 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
212 65          70          75          80

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213 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
214      85      90      95
215 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
216      100     105     110
217 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
218      115     120     125
219 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
220      130     135     140
221 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
222 145      150     155     160
223 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
224      165     170     175
225 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
226      180     185     190
227 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
228      195     200     205
229 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
230      210     215     220
231 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
232 225      230     235     240
233 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
234      245     250     255
235 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
236      260     265     270
237 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
238      275     280     285
239 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
240      290     295     300
241 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
242 305      310     315     320
243 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
244      325     330     335
245 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
246      340     345     350
247 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
248      355     360     365
249 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
250      370     375     380
251 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
252 385      390     395     400
253 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
254      405     410     415
255 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
256      420     425     430
257 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
258      435     440     445
259 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
260      450     455     460
261 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu

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VERIFICATION SUMMARY

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L:44 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1

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L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2